



US-09-768-781-2 (1-1389) x US-09-768-781-4 (1-462)

Qy 1 ATGACACAGACCAACATTCAGAAAGAACCTCGACAATGGACAGAGTTTATGAAATT 60  
Db 1 MetAenThrArgProGlnHisSerGluArgThrSerThrMetAspArgValTyrGluIle 20  
Qy 61 CCTGAGGAGCCAAATGTGATCCGGTTTCATCTCTGGAGGAGATGTCTATCCGTGGAGCC 120  
Db 21 ProGluGluProAsnValAspProValSerSerLeuGluGluAspValIleArgGlyAla 40  
Qy 121 AACCCCGGATTTACTTTTCCATTTAGCATCTCTTTTCCACCTTTTGTACTGTGGGAG 180  
Db 41 AsnProArgPheThrPheProPheSerIleLeuPheSerThrPheLeuTyrCysGlyGlu 60  
Qy 181 GCTGCATCTGTTGTACATGTTAGATCTATCGAAGAATAGTGAACCTACTGGATG 240  
Db 61 AlaAlaSerAlaLeuTyrMetValArgIleTyrArgLysAsnSerGluThrTyrTrpMet 80  
Qy 241 ACATACACCTTTTCTTTCTTTATGTTTTCATCCATATGTTCCAGTTCACCTCATTTT 300  
Db 81 ThrTyrThrPheSerPhePheMetPheSerIleMetValGlnLeuThrLeuIlePhe 100  
Qy 301 GTCCACAGAGATCTAGCCAAAGATAAACCGCTATCATTTATGATCATCTAATCTCTTG 360  
Db 101 ValHisArgAspLeuAlaLysAspLysProLeuSerLeuPheMetHisLeuIleLeuLeu 120  
Qy 361 GGACCTGTTATCAGATGTTTGAGGCCATGATTAAAGTACCTCACACTGTGGAAGAAAGAG 420  
Db 121 GlyProValIleArgCysLeuGluAlaMetIleLysTyrLeuThrLeuTyrLysLysGlu 140  
Qy 421 GAGCAGGAGGCCCTATGTGAGCTCACCAGAAAGAGATGCTAATAGATGGCGAGAG 480  
Db 141 GluGlnGluProTyrValSerLeuThrArgLysLysMetLeuIleAspGlyGluGlu 160  
Qy 481 GTGCTGATAGAAATGGAGGTGGGCACCTCCATCCGAGCCCTGGCTATCACCGCAATGCC 540  
Db 161 ValLeuIleGluThrGluValGlyHisSerIleArgThrLeuAlaMetHisArgAsnAla 180  
Qy 541 TACAAACGTATGTACAGATCCAAAGCCTTCTCGGCTCAGTGCCCGACCTGACCTATCAG 600  
Db 181 TyrLysArgMetSerGlnIleGlnAlaPheLeuGlySerValProGlnLeuThrTyrGln 200  
Qy 601 CTCTATGTGACCTGATCTCTGCAGAGTTCCTCCCTGGGTAGATGTGCTAATGGTATT 660  
Db 201 LeuTyrValSerLeuIleSerAlaGluValProLeuGlyArgValValLeuMetValPhe 220  
Qy 661 TCCCTGGTATCTGTACACCTATGGGCCACCTTTCATATGTTGGCTATCCAGATCAAG 720  
Db 221 SerLeuValSerValThrTyrGlyAlaThrLeuCysAsnMetLeuAlaIleGlnIleLys 240  
Qy 721 TACGATGACTACAAGATTCGCTTGGGCCACTAGAAAGTCTCTGTGCATCACCATCTGGCGG 780  
Db 241 TyrAspAspTyrLysIleArgLeuGlyProLeuGluValLeuCysIleThrIleTrpArg 260  
Qy 781 ACATTGGAGATCACTTCCCGCTCTGATTTGTTGGTCTCTCTCAGCCACTTTGAAATTG 840  
Db 261 ThrLeuGluIleThrSerArgLeuLeuIleLeuValLeuPheSerAlaThrLeuLysLeu 280  
Qy 841 AAGCTGTGCCCTTCTAGTGTCACTTCTGATCATCTCTTGTAGCCCTTGGATTAAG 900  
Db 281 LysAlaValProPheLeuValLeuAsnPheLeuIleIleLeuPheGluProTrpIleLys 300  
Qy 901 TTCTGGAGAGTGTGGCCAGATGCCCAATAACATTTAGAAAAAATTCAGCCGGGTCCGC 960  
Db 301 PheTrpArgSerGlyAlaGlnMetProAsnIleGluLysAsnPheSerArgValGly 320  
Qy 961 ACTCTGGTGTCTGATTTAGTACCATCTCTATGCTGATGATCACTCTCTTCTGCTGG 1020  
Db 321 ThrLeuValValLeuIleSerValThrIleLeuTyrAlaGlyIleAsnPheSerCysTrp 340  
Qy 1021 TCAGCTTGCAGTTGAGCTGGCAGACAGATCTCTCGACAAAGGCGCAGACTGGGA 1080  
Db 341 SerAlaLeuGlnLeuArgLeuAlaAspArgLeuValAspLysGlyGlnAsnTrpGly 360

Qy 1081 CATATGGCCCTGCACTATAGTGTGAGTTGCTAGAGAAATGTGATCATGCTCTGTTTTT 1140  
Db 361 HisMetGlyLeuHisTyrSerValArgLeuValGluAsnValIleMetValLeuValPhe 380  
Qy 1141 AAGTTCTTTGAGTGAAAGTGTACTGAATTAATCTGATTCATCTCTGATTCCTTCAGCTC 1200  
Db 381 LysPhePheGlyValLysValLeuLeuAsnTyrCysHisSerLeuIleAlaLeuGlnLeu 400  
Qy 1201 ATTATGCTTATCTGATTTCCATTGGCTTCCATGCTCTCTTTCTTCCAGTACTTGATCCA 1260  
Db 401 IleIleAlaTyrLeuIleSerIleGlyPheMetLeuLeuPhePheGlnTyrLeuHisPro 420  
Qy 1261 TTGGCTCACTCTTCCACCCATAATGTAAGTACTAGTACTACCTCCATTGCTGCTGCTCACCAG 1320  
Db 421 LeuArgSerLeuPheThrHisAsnValValAspTyrLeuHisCysValCysCysHisGln 440  
Qy 1321 CACCTCGGACGAGGTGAGAACTCAGAGCCACCTTTGAGACTGAAAGCAAGGCAAACT 1380  
Db 441 HisProArgThrArgValGluAsnSerGluProPheGluThrGluAlaArgGlnSer 460  
Qy 1381 GTTGTCT 1386  
Db 461 ValVal 462

RESULT 2  
US-09-768-781-7  
; Sequence 7, Application US/09768781  
; Patent No. US20020142376A1  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV, Gennady V. et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001057-CIP  
; CURRENT APPLICATION NUMBER: US/09/768,781  
; CURRENT FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-09-768-781-7

Alignment Scores:  
Pred. No.: 4,94e-220 Length: 449  
Score: 2322.00 Matches: 449  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 91.31% Indels: 0  
DB: 10 Gaps: 0

US-09-768-781-2 (1-1389) x US-09-768-781-7 (1-449)

Qy 40 ATGACAGAGTTTATGAAATTCCTGAGAGGCCAAATGTGATCCCGTTTCATCTCTGGAG 99  
Db 1 MetAspArgValTyrGluIleProGluGluProAsnValAspProValSerLeuGlu 20  
Qy 100 GAAGATGTCATCCGTGGAGCCAAACCCCGATTACTTTTCCATTAGCATCTTTTCTCC 159  
Db 21 GluAspValIleArgGlyAlaAsnProArgPheThrPheProPheSerIleLeuPheSer 40  
Qy 160 ACCTTTTTGTACTGTGGGAGCGCTGCTCTGTTGTATGATGTTAGATCTATCGAAAG 219  
Db 41 ThrPheLeuTyrCysGlyGluAlaAlaSerAlaLeuTyrMetValArgIleTyrArgLys 60  
Qy 220 AATAGTGAACCTTACTGGATGACATACACCTTTTCTTTCTTTATGTTTTCATCCATTATG 279  
Db 61 AsnSerGluThrTyrTrpMetThrTyrThrPheSerPhePheMetPheSerSerIleMet 80  
Qy 280 GTCCAGTTGACCCCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCATTA 339



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Db 201 ArgValValLeuMetValPheSerLeuValSerValThrTyrGlyAlaThrLeuCysAsn 220
Qy 700 ATGTGGCTATCCAGATCAAGTACGATGACTACAGATTCGGCTTGGCCACTAGAGTC 759
Db 221 MetLeuAlaIleGlnIleLysTyrAspAspTyrLysIleArgLeuGlyProLeuGluVal 240
Qy 760 CTCTGCATCACCATCTGGCGGACATTTGGAGATCACTTCCCGCTCTCTGATTCGGTGCTC 819
Db 241 LeuCysIleThrIleTyrArgThrLeuGluIleThrSerArgLeuLeuIleValLeu 260
Qy 820 TTCTCAGCAGCTTTGAAATTAAGGCTGTGCGCTTCTCTAGTGTCTCAACTTCTGTATCATC 879
Db 261 PheSerAlaThrLeuLysLeuLysAlaValProPheLeuValLeuAsnPheLeuIle 280
Qy 880 CTCTTGAGCCCTGGATTAAGTCTGGGAGAGTGTGGCCAGATGCCCAATACATTCAG 939
Db 281 LeuPheGluProTyrIleLysPheTyrArgSerGlyAlaGlnMetProAsnAsnIleGlu 300
Qy 940 AAAAATTTCAGCCGGTGGCACTCTGGTGCTCTGATTTTCAGTCCACCATCTCTATGCT 999
Db 301 LysAsnPheSerArgValGlyThrLeuValValLeuIleSerValThrIleLeuTyrAla 320
Qy 1000 GGCATCACTTCTCTGTGCTGTCAGTCTTTCAGTGTGAGTGGCGAGACAGATCTGTCTC 1059
Db 321 GlyIleAsnPheSerCysTyrPheSerAlaLeuGlnLeuArgLeuAlaAspArgAspLeuVal 340
Qy 1060 GACAAAGGCGAGAACTGGGGACATATGGCCCTGCATATAGTGTGAGTGTGGTAGAGAT 1119
Db 341 AspLysGlyGlnAsnTyrPheGlyHisMetGlyLeuHisTyrSerValArgLeuValGluAsn 360
Qy 1120 GTGATCATGTCTTGGTCTTAAAGTCTTGGAGTGAAGTGTACTGAAATTAATCTGTCAT 1179
Db 361 ValIleMetValLeuValPheLysPhePheGlyValLysValLysValLeuLeuAsnTyrCysHis 380
Qy 1180 TCCTTGATGCTTCAGCTCATTAATGCTATCTGATTTCCATTCAGTGTGCTTCTCTCTT 1239
Db 381 SerLeuIleAlaLeuGlnLeuIleAlaTyrLeuIleSerIleAspPheMetLeuLeu 400
Qy 1240 TTCCTCCAGTACTTCATCCATTCGGCTCACTTTCACCCATAATGATAGTACACTACCTC 1299
Db 401 PhePheGlnTyrLeuHisProLeuArgSerLeuPheThrHisAsnValValAspTyrLeu 420
Qy 1300 CATTTGTCTGTCTGCACAGCAGCCTCGACAGGTTGAGAACTTCAGAGCCACCTTT 1359
Db 421 HisCysValCysCysHisGlnHisProArgThrArgValGluAsnSerGluProPhe 440
Qy 1360 GAGACTGAAGCAAGCAAGTGTCTC 1386
Db 441 GluThrGluAlaArgGlnSerValVal 449

RESULT 4
US-09-768-781-6
; Sequence 6, Application US/09768781
; Patent No. US20020142376A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady V. et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001057-CIP
; CURRENT APPLICATION NUMBER: US/09/768, 781
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-768-781-6
Alignment Scores: 2.63e-85 Length: 405
Pred. No.: 953.50 Match: 181
Score:
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Percent Similarity: 64.72% Conservative: 85
Best Local Similarity: 44.04% Mismatches: 134
Query Match: 37.50% Indels: 11
DB: 1.0 Gaps: 4
US-09-768-781-2 (1-1389) x US-09-768-781-6 (1-405)
Qy 136 TTTCCATTAGCATCTTTTCTCCACCTTTTGTACTGTGGGAGGCTCATCTGCTTTG 195
Db 1 PheProAlaSerValIleAlaSerValPheLeuPheValAlaGluThrAlaAlaLeu 20
Qy 196 TACATGGTTAGAAATATATCGAAAGAATAGTGAACCTTACTGGATGACATACACCTTTCT 255
Db 21 TyrLeuSerSerThrTyrArgSerAlaGlyAspArgMetTyrGlnValLeuThrLeuLeu 40
Qy 256 TTCCTTATGTTTTCATCCATTATGTCATGTCAGTTCAGCTCATTTTGTCCACAGATCTTA 315
Db 41 PheSerLeuMetProCysAlaLeuValGlnPheThrLeuLeuPheValHisArgAspLeu 60
Qy 316 GCRAAGATAAACCGCTATCATTTATTTATGATCTAATCTCTTGGGACCTGTATCAGA 375
Db 61 SerArgAspArgProLeuAlaLeuLeuMetHisLeuLeuGlnLeuGlyProLeuTyrArg 80
Qy 376 TGTTTGGAGGCCATGATTAAGTACCTCACACTGTGGAGAAAGAGAGGAGGAGGAGCCCC 435
Db 81 CysCysGluValPheCysIleTyrCys-----GlnSerAspGlnAsnGluPro 97
Qy 436 TATGTACGCTCACCAGAAAGAG---ATGCTAATAGATGGCGAGGAGGTGCTGTATAGAA 492
Db 98 TyrValSerIleThrLysLysArgGlnMetProLysAspGlyLeuSerGluGluValGlu 117
Qy 493 TGGGAGGTGGGCCACTCCATCCGGACCTGGCTATGCACCGCAATCCCTACAAACCTATG 552
Db 118 LysGluValGlyGlnAlaGluGlyLysLeuIleThrHisArgSerAlaPheSerArgAla 137
Qy 553 TCACAGATCCAGACCTCTCTGGGTCAGTCCCGCAGCTGACCTATCAGCTCTGTATGTAGC 612
Db 138 SerValIleGlnAlaPheLeuGlySerAlaProGlnLeuThrLeuGlnLeuTyrIleThr 157
Qy 613 CTGATCTCTGACAGGTTCCCTGGGTAGAGTTGTCTAATGGTATTTTCCCTGGTATCT 672
Db 158 ValLeuGluGlnAsnIleThrThrGlyArgCysPheIleMetThrLeuSerLeuLeuSer 177
Qy 673 CTCACCTATGGGCCACCTTTTGCATATGTTGGTATCCAGATCAAGTACGATGACTAC 732
Db 178 IleValTyrGlyAlaLeuArgCysAsnIleLeuAlaIleLysIleLysTyrAspGluTyr 197
Qy 733 AAGATTCCGCTTGGGCCACTAGAGTCTCTGTCATCCATCTGGCGGACATTGGAGATC 792
Db 198 GluValLysValLysProLeuAlaTyrValCysIlePheLeuTyrArgSerPheGluIle 217
Qy 793 ACTTCCCGCTCTGATTCGTGCTCTTCTCAGCCACTTTGAAATTTGAAGCTGTGCGCC 852
Db 218 AlaThrArgValIleValLeuValLeuPheThrSerValLeuLysIleTyrValValAla 237
Qy 853 TTCCTAGTGTCAACTTCTGATCATCTCTTTGAGCCCTGATTAAGTTCTTGGAGAAGT 912
Db 238 ValIleLeuValAsnPhePheSerPheLeuTyrProTyrIleValPheTyrCysSer 257
Qy 913 GGTGCCAGATGCCCAATAACATTTCAGAAAAAACTTCAGCCGGTGGGCACTCTGGTGGTC 972
Db 258 GlySerProPheProGluAsnIleGluLysAlaLeuSerArgValGlyThrThrIleVal 277
Qy 973 CTGATTTTCAGTCAACATCTCTATCTGTCATCAACTTCTCTTGTGTGTGAGTTCGAG 1032
Db 278 LeuCysPheLeuThrLeuLeuTyrAlaGlyIleAsnMetPheCysTyrPheSerAlaValGln 297
Qy 1033 TTGAGTTGGCAGACAGATCTCTGCACAAAGGCGAAGTGGGACATATGCGCCTG 1092
Db 298 LeuLysIleAspAsnProGluLeuIleSerLysSerGlnAsnTyrPheArgLeuLeuIle 317
Qy 1093 CACTATAGTGTGAGTGTGAGAGATGTGATCATGTGCTTCTGTTTAAAGTCTTCTTGA 1152
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; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006677
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006684
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006699
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine
; SEQ ID NO 37894
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007064.22
; OTHER INFORMATION: EXPRESSED IN HEART, S
; OTHER INFORMATION: EXPRESSED IN BRAIN, S
; OTHER INFORMATION: EST HUMAN HIT: AA32560
; OTHER INFORMATION: SWISSPROT HIT: P51811
; US-09-864-761-37894

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Alignment Scores:		
Pred. No.:	3,878-27	128
Score:	361.00	66
Percent Similarity:	81.6%	Conservative: 23
Best Local Similarity:	60.5%	Mismatches: 20
Query Match:	14.20%	Indels: 0
DB:	10	Gaps: 0

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 3.3  
; OTHER INFORMATION: EST HUMAN HIT: A1697050.1, EVALUE 6.00e-43  
; OTHER INFORMATION: SWISSPROT HIT: P51811, EVALUE 1.00e-43  
US-09-864-761-35764

## Alignment Scores:

Pred. No.: 7,81e-09 Length: 86  
Score: 174.50 Matches: 39  
Percent Similarity: 69.86% Conservative: 12  
Best Local Similarity: 53.42% Mismatches: 21  
Query Match: 6.86% Indels: 1  
DB: 10 Gaps: 1

US-09-768-781-2 (1-1389) x US-09-864-761-35764 (1-86)

QY 427 GAGGAGCCCTATGTGACCTCACCGAAGAG---ATGCTAATAGATGGCGAGGAGTG 483  
DB 14 GluGluProTyrValSerIleThrLysArgGlnMetProLysAsnGlyLeuSerGlu 33  
QY 484 CTGATAGATGGAGGTGGCCACTCCATCGGACCCCTGGCTATGCACCGCAATCGCTAC 543  
DB 34 GluIleGluLysGluValGlyGlnAlaGluGlyLysLeuIleThrHisArgSerAlaPhe 53  
QY 544 AAAGCTATGTCCACAGATCCAGACCTTCTCTGGGCTCAGTGGCCCGACCTGACCTATCAGCTC 603  
DB 54 SerArgAlaSerValIleGlnAlaPheLeuGlySerAlaProGlnLeuThrLeuGlnLeu 73  
QY 604 TATGTAGCTGATCTCTGCAGAGGTTCCCTGGGTAGA 642  
DB 74 TyrIleSerValMetGlnGlnAspValThrValGlyArg 86

## RESULT 10

US-10-174-590-524  
; Sequence 524, Application US/10174590  
; Publication No. US20030008352A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETS AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C42  
; CURRENT APPLICATION NUMBER: US/10/174,590  
; CURRENT FILING DATE: 2002-06-18  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 524  
; LENGTH: 686  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-174-590-524

## Alignment Scores:

Pred. No.: 0.000748 Length: 686  
Score: 127.00 Matches: 81  
Percent Similarity: 35.94% Conservative: 57  
Best Local Similarity: 21.09% Mismatches: 158  
Query Match: 4.99% Indels: 88

DB: 9 Gaps: 15  
US-09-768-781-2 (1-1389) x US-10-174-590-524 (1-686)  
QY 157 TCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTACATGTTAGAAATCTATCGA 216  
DB 9 SerAlaLeuLeuGlnAlaAlaGluGlnSerAlaArgLeuTyrThrValAlaTyrTyrPhe 28  
QY 217 AAGAATAGTGAACCTTACTGGATGACATACACCTTTTCTTTCTTTATGTTTTCATCCATT 276  
DB 29 ThrThrGlyArgLeuLeuTyrGlyTyrPheAlaLeuAlaValLeuLeuProGlyPheLeu 48  
QY 277 ATGGTCCAGTTTACCCCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCCTATCA 336  
DB 49 ValGlnAlaLeuSerTyrLeuTyrPheArgAlaAspGlyHisProGlyHisCysSerLeu 68  
QY 337 TATTTATGATCATCTAATCCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAG 396  
DB 69 ValMetLeuHisLeuLeuGlnLeuGlyValTyrPheArgHisTyrPheAspAlaLeuThr 88  
QY 397 TACCTCACACTGTGGAAGAAAGAGGAGGAGGAGCCCTATGTGCAGCCTCACCCGAAAG 456  
DB 89 SerLeu-----GlnLysGlnLeuGlnAlaProHisArgGly----- 100  
QY 457 AAGATGCTAATAGATGGCGAGGCTGCTAGTAATGGAGGTGGGCCACTCCATCCCG 516  
DB 101 -----Tyr----- 101  
QY 517 ACCGTGGCTATGACCGCAATGCCCTACAAACGTATGTACAGATCAACAGCTTCTCTGGGC 576  
DB 102 ---LeuGlnLeuGlnGlnAlaAspLeuSerAlaLeuArgLeuGlnAlaLeuLeuGln 120  
QY 577 TCAGTGGCCCGACCTATCAGCTCTATGTAGCCCTGATCTCTGCAGAGGTTCCTCCCTG 636  
DB 121 ThrGlyProHisLeuLeuGlnLeuGlnThrTyrValPheLeuAlaSerAspPheThrAspIle 140  
QY 637 GGTAGAGTTGTGCTAATGCTATTTTCCCTGTATCTGTACACCTATGTGGGCCACCTTTGC 696  
DB 141 ValProGlyValSerThrLeuPheSerTyrPheSerLeuSerTyrPheAlaLeu----- 157  
QY 697 AATATGTTGGCTATCCAGATCAAGTACGATGACATACAGATTCGCCCTTGGGCA----- 750  
DB 158 -----ValSerTyrThrArgPheMetGlyPheMetLysProGlyHis 171  
QY 751 -----CTAGAAGTCTCTGCATCACCATCTGCGGACATTTGGAGATCACT 795  
DB 172 LeuAlaMetProTyrPheAlaLeuPheCysGlnGlnLeuTyrPheArgMetGlyMetLeuGly 191  
QY 796 TCCGCGCTCTCTGATTCGCTCTCTCAGCCACTTTGAAATTCGAAGCTGTGCCCTTC 855  
DB 192 ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyrHisPhe 206  
QY 856 CTAGTGTCTCAACTTCTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCTGGAGA 909  
DB 207 TrpVal-----PheValValAlaGlyAlaHisTyrPheValMetThrPheTyrLeu 223  
QY 910 AGTGTGCCAGATGCCCAATACATTGAGAAACCTTCAGC---CGGTCCGCACTCTG 966  
DB 224 Val---AlaGlnGlnSerAspIleIleAspSerThrCysHisTyrPheArgLeuPheAsnLeu 242  
QY 967 GTGTGCTGATTTTCACTCAGTCACCATCTCTATGTGGCATCAACTCTCTGTGGTGGT 1026  
DB 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTyrPheSer 258  
QY 1027 TTGCAGTTGAGGTTGGCAGACAGATCTCGTCGACAAAGGCGACAGACTGGGACATATG 1086  
DB 259 -----ProSerArgAsnArgMet 264  
QY 1087 GGCCTGCACTATAGTGTGAGGTGGTAGAATGTGATCATGCTCTGTTTAAAGTTC 1146  
DB 265 ValThrPheTyrMetValMetLeuLeuGlnAlaIleIleLeuLeuLeuAlaThrAsp 284  
QY 1147 TTT-----GGAGTGAAAGTGTACTGAATTACTCTCATTCCTTGTGATTCCTGTCAGCTC 1200



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Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTCATTCAGCTTCCTTTCTTCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTrpSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320

RESULT 11
US-10-176-758-524
; Sequence 524, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; PENDING FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 524
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-524

Alignment Scores:
Pred. No.: 0.000748 Length: 686
Score: 127.00 Matches: 81
Percent Similarity: 35.94% Conservative: 57
Best Local Similarity: 21.09% Mismatches: 158
Query Match: 4.99% Indels: 88
DB: 9 Gaps: 15

US-09-768-781-2 (1-1389) x US-10-176-758-524 (1-686)
QY 157 TCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTACATGGTTAGATCTATCGA 216
Db 9 SerAlaLeuLeuGlnAlaGlnSerAlaArgLeuTyrThrValAlaTyrTrpPhe 28
QY 217 AAGAATAGTGAACCTACTGATGACATACACCTTTCTTTCTTTATGTTTCATCATT 276
Db 29 ThrThrGlyArgLeuLeuTrpGlyTrpLeuAlaLeuAlaValLeuLeuProGlyPheLeu 48
QY 277 ATGGTCAGTTGACCTTCATTTTGTGCACAGATCTAGCCAAAGATAAACCGCTATCA 336
Db 49 ValGlnAlaLeuSerTyrLeuTrpPheArgAlaSerGlyHisProGlyHisCysSerLeu 68
QY 337 TTATTTATGATCTTAATCTCTTTGGGACCTGTTATCATGATGTTTGGAGGCCATGATTAAG 396
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaAlaLeuThr 88
QY 397 TACCTCACACTGTGGAAGAAGAGGACGAGGAGCCCTATGTGACCTCACCCGAAAG 456
Db 89 SerLeu-----GlnLysGluLeuGlnAlaProHisArgGly----- 100
QY 457 AAGATGCTAATAGATGCGGAGGAGTGTGTATAGTAAGTGGGAGGTGGGCCACTCCATCGG 516
Db 101 -----Trp----- 101
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QY 517 ACCGTGGCTATGCACCGCAATGCCTACAAACGTATGTACAGATCCAAAGCCTTCCTGGGC 576
Db 102 ---LeuGlnLeuGlnGlnAlaAspLeuSerAlaLeuArgLeuLeuGlnAlaLeuGln 120
QY 577 TCAGTGGCCCGAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCTGTGAGAGGTTCCTCG 636
Db 121 ThrGlyProHisLeuLeuGlnThrTyrValPheLeuAlaSerAspPheThrAspIle 140
QY 637 GGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTACCTATGCGGGCCACCTTTGC 696
Db 141 ValProGlyValSerThrLeuPheSerTrpSerLeuSerTrpAlaLeu----- 157
QY 697 AATATGTTGGCTATCCAGATCAAGTCAGTCAGTACAAAGATTTCGCTTGGGCCA----- 750
Db 158 -----ValSerTyrThrArgPheMetGlyPheMetLysProGlyHis 171
QY 751 -----CTAGAAGTCTCTGCATCACCATCTCGCGGACATCTGGAGATCACT 795
Db 172 LeuAlaMetProTrpAlaAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191
QY 796 TCCGCTCTCTGATTCGTGCTCTCTCTCAGCCACTTGAATTTGAAGCTGTGCCTTC 855
Db 192 ThrArgValLeuSerLeuValPhe-----TyrLysAlaTyrHisPhe 206
QY 856 CTAGTGTCAACTTCTCTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCCTGGAGA 909
Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
QY 910 AGTGTGCTCCAGATGCCCAATACATTCAGAAACATTCACG---CGGTGCGGACTCTG 966
Db 224 Val---AlaGlnGlnSerAspIleIleAspSerThrCysHisTrpArgLeuPheAsnLeu 242
QY 967 GTGTCTCTGATTCAGTCACCATCTCTCTGCTGGCATCAACTCTCTGTGCTGCTCAGCT 1026
Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTrpAspSer 258
QY 1027 TTGCAGTTGAGGTTGGCAGACAGAGATCTCTGCACAAAGGCGACAGCTGGGACATATG 1086
Db 259 -----ProSerArgAsnArgMet 264
QY 1087 GGCCTGCATATAGTGTGAGGTTGGTAGAATGTGATCATGTGCTTGGTTTAAAGTTC 1146
Db 265 ValThrPheTyrMetValMetLeuLeuGlnAlaSerIleLeuLeuLeuAlaThrAsp 284
QY 1147 TTT-----GGAGTGAAGTGTACTGAATTCATCTCTGTCATCTCCTTGATTCCTTGAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTCCATTGGCTTCATGCTCTCTTTCTTCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTrpSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320

RESULT 12
US-10-175-737-524
; Sequence 524, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

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; ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; ; FILE REFERENCE: P3430R1C50
; ; CURRENT APPLICATION NUMBER: US/10/175,737
; ; CURRENT FILING DATE: 2002-06-19
; ; Prior Application removed - See File Wrapper or Palm
; ; NUMBER OF SEQ ID NOS: 612
; ; SEQ ID NO 524
; ; LENGTH: 686
; ; TYPE: PRT
; ; ORGANISM: Homo Sapien
US-10-175-737-524

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Alignment Scores:		
Pred. No.:	0.000748	686
Score:	127.00	81
Percent Similarity:	35.94%	Conservative: 57
Best Local Similarity:	21.09%	Mismatches: 158
Query Match:	4.99%	Indels: 88
DB:	9	Gaps: 15

US-09-768-781-2 (1-1389) x US-10-175-737-524 (1-686)

QY	157	TCACACCTTTTGTACTGCGGGAGGCATCTGCCTTTGTACATGATTAGAATCTATAACA	216
DB	9	SerAlaLeuLeuGlnAlaAaGluInSerAlaArgLeuTyThrValAlaTyTyTrpPhe	28
QY	217	AAGNATAGTGAAACTTACTCGATGCACATACACCTTTTCTTCTTTATGTTTTCATCCATT	276
DB	29	ThrThrglyArgLeuLeuTrpGlyTrpLeuAlaLeuAlaValLeuLeuProGlyPheLeu	48
QY	277	ATGTCGCCAGTTGACCTCATTTTTTGTCCACAGAGATCTAGCCAAAAGATAAACCGCTATCA	336
DB	49	ValClnAlaLeuSerTyLeuTrpPheArgAlaAspGlyHisProGlyHisCysSerLeu	68
QY	337	TATATTATGCATCTAATCCCTCTTTGGGACCTGTTATCAGATGTTTGAGGCCATGATTAAAG	396
DB	69	ValMetLeuHisLeuLeuGlnLeuGlyValTrpIysArgHisTrpAspAlaAlaLeuThr	88
QY	397	TACCTCACACTGTGGGAAGAAGAGGACGAGAGCCCTATCTCAGCCTCACCCGAAAG	456
DB	89	SerLeu-----GlnLysGluLeuGluAlaProHisArgGly-----	100
QY	457	AAGATGCTAATAGATGCCGAGGAGTGCTGCTAGAAATGGGAGGTGGGCCCATCCATCCGG	516
DB	101	-----Trp-----	101
QY	517	ACCCTGCTATGCAACCACCAATGCTACAAAAGTATGTCACAGATCCAAGCTTCCTGGGC	576
DB	102	--LeuGlnLeuGlnGluAlaAaspLeuSerAlaLeuArgLeuLeuGluAlaLeuGln	120
QY	577	TCAGTGGCCCCAGCTGACCTATCAGCTCTATGTGAGGCTGATCTCGACAGGTTTCCCCTG	636
DB	121	ThrGlyProHisLeuLeuLeuGlnThrTy-ValPheLeuAlaSerAspPheThrAspIle	140
QY	637	GGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCCACTATGGGGCCACCCTTCG	696
DB	141	ValProGlyValSerThrLeuPheSerTrpSerSerLeuSerTrpAlaLeu-----	157
QY	697	AATATGTTGGCTATCCAGATCAAGATCAGTACGATCTACAAGATTTCGCTTGGGCCA----	750
DB	158	-----ValSerTyThrArgPheMetGlyPheMetIysProGlyHis	171
QY	751	-----CTAAGAGTCCTTCGCATCACCATCGGCGGCACATTTGGAGATCACT	795
DB	172	LeuAlaMetProTrpAlaAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly	191
QY	796	TCCGGCTCTGATTCGTGGTCTCTTCACGCCACTTTGAAATTGAAGGCTGTGCCCTTC	855
DB	192	ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyHisPhe	206
QY	856	CTAGTGTCTCAACTCTTCGTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCTGGAGA	909

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Db      207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
Qy      910 AGTGGTGGCCAGATGCCCAATAACATTGAGAAAAACTTTTCAGC---CGGGTCGGCACTCTG 966
Db      224 Val---AlaGlnSerAspIleIleAspSerThrCysHisTrpArgLeuPheAsnLeu 242
Qy      967 GTGGTCTCTGATTTCAAGTCACCAATCCTCTATGTGGTCATCAACTCTCTCTTGTGTGGTCAGCT 1026
Db      243 LeuValGlyAlaValIlyrIleLeuCysTyr-----LeuSerPheTrpAspSer 258
Qy      1027 TTGCAGTTGAGGTTGGCAGACAGAGATCTCGTGACAAGGGCAGAACTGGGGACATATG 1086
Db      259 -----ProSerArgAsnArgMet 264
Qy      1087 GGCGTCGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGCTGTGGTTTTTAAGTTTC 1146
Db      265 ValThrPheTyrMetValMetLeuLeuGluAsnIleIleLeuLeuLeuAlaThrAsp 284
Qy      1147 TTT-----GGAGTGAAGCTGTACTGAATTACTGTCTATTCCTTGATTTGCCCTTCAGCTC 1200
Db      285 PheLeuGlnGlyAla-----SertTrpThrSerLeuGlnThr 296
Qy      1201 ATTATT-----GCTTATCTGATTTCCATTTGCTTCATGCTCTCTTTCTTCAG 1248
Db      297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIlyrTyrSer 316
Qy      1249 TACTTGCATCCA 1260
Db      317 LeuLeuHisPro 320

RESULT 13
US-10-173-706-524
; Sequence 524, Application US/10173706
; Publication No. US2003002293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ. ID. NO 524
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-524

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Alignment Scores:		
Pred. No.:	0.000748	Length:
Score:	127.00	Matches:
Percent Similarity:	35.94%	Conservative:
Best Local Similarity:	21.09%	Mismatches:
Query Match:	4.99%	Indels:
DB:	9	Gaps:
		DB:

US-09-768-781-2 (1-1389) x US-10-173-706-524 (1-686)

QY 157 TCACACCTTTTGTACTGTGGGAGGTGCATCTGCTTTGTACATGGTTAGAATCTATCGA 216

pb 9 SerAlaIeuLeuGlnAlaLaGluGlnSerAlaArqLeuTyrThrValAlaTyrTyrPhe 28

QY 217 AAGATAGTGAACTTACTGGATGACATACACCTTTCTTTCTTTATGTTTTCATCATT 276  
Db 29 ThrThrGlyArgLeuLeuTrpGlyTrpLeuAlaLeuValLeuLeuProGlyPheLeu 48  
QY 277 ATGGTCCAGTTCACCTTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCA 336  
Db 49 ValGlnAlaLeuSerTyxLeuTrpPheArgAlaAspGlyHisProGlyHisCysSerLeu 68  
QY 337 TTATTATCATCTAATCTCTTGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAAG 396  
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaLeuThr 88  
QY 397 TACCTCACACTGTGGAAGAAGAGGAGGAGGAGCCCTATCTCAGCCTCACCCGGAAG 456  
Db 89 SerLeu-----GlnLysGluLeuAlaProHisArgGly----- 100  
QY 457 AAGATGCTAATAGATGCGGAGGAGGTGCTGATAGAATGGGAGGTGGGCCACTCCATCCGG 516  
Db 101 -----Trp----- 101  
QY 517 ACCCTGGCTATGACCGCAATGCTTCAACAGTATGTACAGATCCAAAGCTTCCTGGGC 576  
Db 102 ---LeuGlnLeuGlnAlaLeuSerAlaLeuArgLeuLeuGlnAlaLeuLeuGln 120  
QY 577 TCAGTGGCCCGACCTGACCTATCAGCTCTATGAGGCTGATCTCTGAGAGGTTCCCGTG 636  
Db 121 ThrGlyProHisLeuLeuGlnThrTyxValPheLeuAlaSerAspPheThrAspIle 140  
QY 637 GGTAGAGTTGTCTAATGTTATTTCCCTGTTATCTGTACCTACCTATGGGCCACCTTTGC 696  
Db 141 ValProGlyValSerThrLeuPheSerTrpSerLeuSerTrpAlaLeu----- 157  
QY 697 AATATGTTGGCTATCCAGCAATCAAGTACAGTACTCAAGATTCGCCTTGGGCA----- 750  
Db 158 -----ValSerTyxThrArgPheMetGlyPheMetLysProGlyHis 171  
QY 751 -----CTAAGTCTCTGATCACCATCCTGCGGACATGCGGACATGGAGTCT 795  
Db 172 LeuAlaMetProTrpAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191  
QY 796 TCCCGCTCTGATCTGTGCTCTTCTCAGCCACTTTGAAATTTGAAGCTGTGCTTTC 855  
Db 192 ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyxHisPhe 206  
QY 856 CTAGTGCTCAACTCTCTGATCTCTCTTTGAGCCCTGGATT-----AAGTCTCTGAGA 909  
Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223  
QY 910 AGTGTGCGCAGATGCCCAATTAACATTGAGAAAACCTCAGC---CGGTGCGCCTCTG 966  
Db 224 Val---AlaGlnGlnSerAspIleLeuAspSerThrCysHisTrpArgLeuPheAsnLeu 242  
QY 967 GTGTCCTGATTTAGTACCTCCTATGCTGGATCACTTCTCTGCTGCTCAGCT 1026  
Db 243 LeuValGlyAlaValTyxIleLeuCysTyx-----LeuSerPheTrpAspSer 258  
QY 1027 TTGCAGTTGAGGTGTGGACACAGATCTCTGTCGCAAAAGGCGAGATGGGGACATATG 1086  
Db 259 -----ProSerArgAsnArgMet 264  
QY 1087 GGCCTGCATATAGTGTGAGGTGTGAGAGATGTGATCATGCTCTGTTGTTTAAAGTTC 1146  
Db 265 ValThrPheTyxMetValMetLeuLeuGlnAlaAsnIleLeuLeuLeuAlaThrAsp 284  
QY 1147 TTT-----GGAGTGAAGTGTACTGAATTACTGTCTTCTGATTCCTGCTGAGCTC 1200  
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296  
QY 1201 ATTATT-----GCTATCTGATTTCCATTGGCTTCATGCTCTTCTTCTCCAG 1248  
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyxSer 316  
QY 1249 TACTTGCATCCA 1260

Db 317 LeuLeuHisPro 320  
RESULT 14  
; Sequence 524, Application US/10175738  
; Publication No. US2003002294A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P34301C45  
; CURRENT APPLICATION NUMBER: US/10/175,738  
; CURRENT FILING DATE: 2002-06-19  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 524  
; LENGTH: 686  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-175-738-524  
Alignment Scores:  
Pred. No.: 0.000748 Length: 686  
Score: 127.00 Matches: 81  
Percent Similarity: 35.94% Conservative: 57  
Best Local Similarity: 21.09% Mismatches: 158  
Query Match: 4.99% Indels: 88  
DB: 9 Gaps: 15  
US-09-768-781-2 (1-1389) x US-10-175-738-524 (1-686)  
QY 157 TCACCTTTTGTACTGTGGGAGGTGCATCTGCTTTGTACATGTTTGTAGTATCTATCGA 216  
Db 9 SerAlaLeuLeuGlnAlaGlnSerAlaArgLeuTyxValAlaTyxPhe 28  
QY 217 AAGATAGTGAACTTACTGGATGACATACACCTTTCTTTCTTTATGTTTTCATCATT 276  
Db 29 ThrThrGlyArgLeuLeuTrpGlyTrpLeuAlaLeuValLeuLeuProGlyPheLeu 48  
QY 277 ATGGTCCAGTTCACCTTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCA 336  
Db 49 ValGlnAlaLeuSerTyxLeuTrpPheArgAlaAspGlyHisProGlyHisCysSerLeu 68  
QY 337 TTATTATCATCTAATCTCTTGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAAG 396  
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaLeuThr 88  
QY 397 TACCTCACACTGTGGAAGAAGAGGAGGAGGAGCCCTATCTCAGCCTCACCCGGAAG 456  
Db 89 SerLeu-----GlnLysGluLeuAlaProHisArgGly----- 100  
QY 457 AAGATGCTAATAGATGCGGAGGAGGTGCTGATAGAATGGGAGGTGGGCCACTCCATCCGG 516  
Db 101 -----Trp----- 101  
QY 517 ACCCTGGCTATGACCGCAATGCTTCAACAGTATGTACAGATCCAAAGCTTCCTGGGC 576  
Db 102 ---LeuGlnLeuGlnAlaLeuSerAlaLeuArgLeuLeuGlnAlaLeuLeuGln 120  
QY 577 TCAGTGGCCCGACCTGACCTATCAGCTCTATGAGGCTGATCTCTGAGAGGTTCCCGTG 636  
Db 121 ThrGlyProHisLeuLeuGlnThrTyxValPheLeuAlaSerAspPheThrAspIle 140

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QY 637 GGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTACACCTATGGGGCCACCTTTTGC 696
Db 141 ValProGlyValSerThrLeuPheSerTrpSerSerLeuSerTrpAlaLeu----- 157
QY 697 AATATGTTGGCTATCCAGATCAAGTACAGTACACTACAAGATTCGCGCTTGGGCCA----- 750
Db 158 -----ValSerTyrThrArgPheMetGlyPheMetLysProGlyHis 171
QY 751 -----CTAGAAGTCTCTGCATCACACTCTGGCGGACATTTGGAGATCACT 795
Db 172 LeuAlaMetProTrpAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191
QY 796 TCCGCGCTCTCTGATTTCTGGTCTCTTCTCAGCCACTTTGAAATTTGAAGCTGTGCGCTTC 855
Db 192 ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyrHisPhe 206
QY 856 CTAGTGCTCAACTTCTCTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCTGGAGA 909
Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
QY 910 AGTGGTCCCGAGTCCCAATAACATTGAGAAAACTTCAGC---CGGGTCGGCACTCTG 966
Db 224 Val---AlaGlnGlnSerAspIleAspSerThrCysHisTrpArgLeuPheAsnLeu 242
QY 967 GTGCTCTGATTTCAGTCACCATCTCTATGCTGGCATCACTTCTTCTGCTGGTCAGCT 1026
Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTrpAspSer 258
QY 1027 TTGCAGTTTGAGTTGGCAGACAGAGATCTCGTCGACAAAGGCGCAACTGGGGACATATG 1086
Db 259 -----ProSerArgAsnArgMet 264
QY 1087 GGCTGTGCACTATAGTGTGAGTGTGTGAGAGATGTGATCTGTCTGTTTAAAGTTC 1146
Db 265 ValThrPheTyrMetValMetLeuLeuGluAsnIleLeuLeuLeuAlaThrAsp 284
QY 1147 TTT-----GGAGTGAAGTGTACTGAATCTGATCTGATCTGCTTTCCTGAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTTCCATTCTGCTTTCATGCTTCTCTTCTTCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTrpSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320

RESULT 15
US-10-175-752-524
; Sequence 524, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Par, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC80
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 524
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; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-524

Alignment Scores:
Pred. No.: 0.000748 Length: 686
Score: 127.00 Matches: 81
Percent Similarity: 35.94% Conservative: 57
Best Local Similarity: 21.09% Mismatches: 158
Query Match: 4.99% Indels: 88
DB: 9 Gaps: 15

US-09-768-781-2 (1-1389) x US-10-175-752-524 (1-686)
QY 157 TCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTGTACATGGTTAGATCTATCA 216
Db 9 SerAlaLeuLeuGlnAlaAlaGlnSerAlaArgLeuTyrThrValAlaTyrTyrPhe 28
QY 217 AAGAATAGTGAACCTTACTGGATGACATACACCTTTTCTTTCTTTTATGTTTTCATCCATT 276
Db 29 ThrThrGlyArgLeuLeuTrpGlyTrpLeuAlaLeuAlaValLeuLeuProGlyPheLeu 48
QY 277 ATGTCTCCAGTTTGACCTCATTTTGTCTCCACAGAGATCTAGCCAAAGATAAACCGCTATCA 336
Db 49 ValGlnAlaLeuSerTyrLeuTrpPheArgAlaAspGlyHisProGlyHisCysSerLeu 68
QY 337 TTATTTATGATCAATACCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAAG 396
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaAlaLeuThr 88
QY 397 TACCTCACACTGTGGAAGAAAGAGAGAGGAGGAGGAGCCCTATGTGAGCCTCACCCGAAG 456
Db 89 SerLeu-----GlnLysGlnLeuGluAlaProHisArgGly----- 100
QY 457 AAGATGCTAATAGTAGTGGCAGAGGTGCTGATAGAATGGAGGTGGGCCACTCCATCCGG 516
Db 101 -----Trp----- 101
QY 517 ACCCTGGCTATGACCGCAATGCCCTACAAAGTATGTACACAGATCCAAAGCTTCCTGGGC 576
Db 102 ---LeuGlnLeuGlnAlaAspLeuSerAlaLeuArgLeuLeuGluAlaLeuLeuGln 120
QY 577 TCAGTGGCCCCAGCTGACCTATCAGCTCTATGTGACCTGATCTCTGCAGAGGTTCCCTCG 636
Db 121 ThrGlyProHisLeuLeuLeuGlnThrTyrValPheLeuAlaSerAspPheThrAspIle 140
QY 637 GGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTACCTATGTGAGGCGGCCACCTTTGC 696
Db 141 ValProGlyValSerThrLeuPheSerTrpSerSerLeuSerTrpAlaLeu----- 157
QY 697 AATATGTTGGCTATCCAGATCAAGTACAGTACACTACAAGATTCGCGCTTGGGCCA----- 750
Db 158 -----ValSerTyrThrArgPheMetGlyPheMetLysProGlyHis 171
QY 751 -----CTAGAAGTCTCTGATCCATCCACTGACCATCTGGCGGACATTTGGAGATCACT 795
Db 172 LeuAlaMetProTrpAlaAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191
QY 796 TCCGCGCTCTCTGATTTCTGGTCTCTTCTCAGCCACTTTTGAATTTGAAGCTGTGCGCTTC 855
Db 192 ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyrHisPhe 206
QY 856 CTAGTGCTCAACTTCTCTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCTGGAGA 909
Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
QY 910 AGTGGTCCCGAGTCCCAATAACATTGAGAAAACTTCAGC---CGGGTCGGCACTCTG 966
Db 224 Val---AlaGlnGlnSerAspIleAspSerThrCysHisTrpArgLeuPheAsnLeu 242
QY 967 GTGCTCTGATTTCAGTCACCATCTCTATGCTGGCATCACTTCTTCTGCTGGTCAGCT 1026
Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTrpAspSer 258
QY 1027 TTGCAGTTTGAGTTGGCAGACAGAGATCTCGTCGACAAAGGCGCAACTGGGGACATATG 1086
Db 259 -----ProSerArgAsnArgMet 264
QY 1087 GGCTGTGCACTATAGTGTGAGTGTGTGAGAGATGTGATCTGTCTGTTTAAAGTTC 1146
Db 265 ValThrPheTyrMetValMetLeuLeuGluAsnIleLeuLeuLeuAlaThrAsp 284
QY 1147 TTT-----GGAGTGAAGTGTACTGAATCTGATCTGATCTGCTTTCCTGAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTTCCATTCTGCTTTCATGCTTCTCTTCTTCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTrpSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320
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Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTyrAspSer 258
QY 1027 TTGCAGTTGAGTTGGCAGACAGAGATCTCGACAAAGGGCAGAACTGGGGACATATG 1086
Db 259 -----ProSerArgAsnArgMet 264
QY 1087 GGCTGCACATAGTGTGAGGTTGGTAGAGAATGTGATCATGTGCTTGGTTTAAAGTTC 1146
Db 265 ValThrPheTyrMetValMetLeuLeuGluAsnIleIleLeuLeuLeuAlaThrAsp 284
QY 1147 TTT-----CGAGTGAAGGTTACTGAATTACTGTCAATTCCTTGATTGCCCTTGAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTyrThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTCCATTGGCTTCATGCTCCTTTCTTCCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTyrSer 316
QY 1249 TACTTGCAATCCA 1260
Db 317 LeuLeuHisPro 320
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Job time : 44.5 secs